

SEQUENCE LISTING

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 Atkinson, Howard
 Neelam, Anil

<120> Plant Cell Death System

<130> 9341-027

<150> 0025225.4
 <151> 2000-10-14

<160> 18

<170> PatentIn Ver. 2.1

<210> 1
 <211> 909
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (1)..(48)
 <223> N-terminal Domain

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 <222> (865)..(903)
 <223> C-terminal Domain

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 <222> (484)..(558)
 <223> Central Domain

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 <222> (226)..(231)
 <223> Sequence replacing removed SacI site

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 <222> (1)..(3)
 <223> Initiation codon added via PCR primer

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 <222> (904)..(909)
 <223> Stop codons added via PCR primer

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 <222> (1)..(24)
 <223> Binding site for primer ProRIPBF

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 <222> (205)..(249)
 <223> Binding site for primer RIPSDF

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 <223> Binding site for primer RIPSDF

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 <223> Binding site for primer ProRIPSR

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 <222> (49)..(73)
 <223> Binding site for primer RIP1BF

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 <222> Complement((837)..(864))
 <223> Binding site for primer RIP2SR

<220>
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 <222> (463)..(579)
 <223> Binding site for primer RIPCDF spanning central domain

<220>
 <221> misc_feature
 <222> Complement((463)..(579))
 <223> Binding site for primer RIPCDF spanning central domain

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 atggccgaga taaccctaga gccgagtgat cttatggcgc aaacaaacaa aagaatagtg 60
 ccaaagttca ctgaaatctt ccccggtggag gacgcgaact acccttacag cgccttcac 120
 gcgtcggtcc ggaaagacgt gatcaaacac tgcaccgacc ataaagggat cttccagccc 180
 gtgctgccac cggagaagaa ggtcccggag ctatggttct acacagaact gaaaactagg 240
 accagctcca tcacgctcgc catacgcatg gacaacctgt acctcgtggg cttcaggacc 300
 ccgggcgggg tgtggtggga gttcggcaag gacggcgaca ccacctcct cggcgacaac 360
 cccaggtggc tcggcttcgg cggcaggtac caggacctca tcggcaacaa gggctctggag 420
 accgtcacca tgggccgcgc cgaaatgacc agggccgtca acgacctggc gaagaagaag 480
 aagatggcga cactggagga ggaggaggtg aagatgcaga tgcagatgcc ggaggccgct 540
 gatctggcgg cggcggcagc ggctgaccca caggccgaca cgaagagcaa gctggtgaag 600

ctggtggtca tgggtgtgca ggggctgcgg ttcaacaccg tgtcccgac ggtggacgcg 660
 gggttcaaca gccagcacgg ggtgaccttg accgtgacgc aggggaagca ggtgcagaag 720
 tgggacagga tctccaaggc ggccttcgag tgggctgacc accccaccgc tgtgatcccc 780
 gacatgcaga agcttggcat caaggataag aacgaagcag cgaggatcgt tgcgctcggt 840
 aagaatcaaa ctactgccgc tgccgctact gctgccagtg ctgacaacga cgacgacgag 900
 gcctaataa 909

<210> 2
 <211> 750
 <212> DNA
 <213> Zea mays

<220>
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 <222> (1)..(3)
 <223> Initiation codon added via PCR primer

<220>
 <221> mutation
 <222> (181)..(186)
 <223> Sequence replacing removed SacI site

<220>
 <221> misc_feature
 <222> (745)..(750)
 <223> Stop codons added by PCR primer

<400> 2
 atgaaaagaa tagtgccaaa gttcactgaa atcttccccg tggaggacgc gaactaccct 60
 tacagcgcct tcatcgcgtc ggtccgaaa gacgtgatca aacactgcac cgaccataaa 120
 gggatcttcc agcccgtgct gccaccggag aagaaggctc cggagctatg gttctacaca 180
 gaactgaaaa ctaggaccag ctccatcacg ctgccatac gcatggacaa cctgtacctc 240
 gtgggcttca ggaccccggg cgggggtgtg tgggagttcg gcaaggacgg cgacaccac 300
 ctctcggcg acaaccccag gtggctcggc ttggcgcca ggtaccagga cctcatcggc 360
 aacaagggtc tggagaccgt caccatgggc cgcgccgaaa tgaccagggc cgtcaacgac 420
 ctggcgaaga agaagaaggc ggctgacca caggccgaca cgaagagcaa gctggtgaag 480
 ctggtggtca tgggtgtgca ggggctgcgg ttcaacaccg tgtcccgac ggtggacgcg 540
 gggttcaaca gccagcacgg ggtgaccttg accgtgacgc aggggaagca ggtgcagaag 600
 tgggacagga tctccaaggc ggccttcgag tgggctgacc accccaccgc tgtgatcccc 660
 gacatgcaga agcttggcat caaggataag aacgaagcag cgaggatcgt tgcgctcggt 720

aagaatcaaa ctactgccgc tgcctaataa

750

<210> 3
<211> 444
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (1)..(3)
<223> Initiation codon added by PCR primer

<220>
<221> mutation
<222> (181)..(186)
<223> Sequence replacing removed SacI site

<220>
<221> misc_feature
<222> (439)..(444)
<223> Stop codons added by PCR primer

<400> 3
atgaaaagaa tagtgccaaa gttcactgaa atcttccccg tggaggacgc gaactaccct 60
tacagcgctt tcatcgcgtc ggtccggaaa gacgtgatca aacactgcac cgaccataaa 120
gggatcttcc agcccggtgct gccaccggag aagaaggctc cgagagctatg gttctacaca 180
gaactgaaaa ctaggaccag ctccatcacg ctcgccatac gcatggacaa cctgtacctc 240
gtgggcttca ggaccccggtg cgggggtgtgg tgggagttcg gcaaggacgg cgacacccac 300
ctcctcggcg acaaccccag gtggctcggc ttcggcggca ggtaccagga cctcatcggc 360
aacaagggtc tggagaccgt caccatgggc cgcgccgaaa tgaccagggc cgtcaacgac 420
ctggcgaaga agaagaagta ataa 444

<210> 4
<211> 354
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (1)..(3)
<223> Initiation codon added by PCR primer

<220>
<221> misc_feature
<222> (349)..(354)
<223> Stop codons added by PCR primer

<400> 4
 atggcggctg acccacaggc cgacacgaag agcaagctgg tgaagctggt ggtcatggtg 60
 tgcgaggggc tgcggttcaa caccgtgtcc cgcacggtgg acgcgggggt caacagccag 120
 cacggggtga ccttgaccgt gacgcagggg aagcaggtgc agaagtggga caggatctcc 180
 aaggcggcct tcgagtgggc tgaccacccc accgctgtga tccccgacat gcagaagctt 240
 ggcataaagg ataagaacga agcagcgagg atcggtgcgc tcgttaagaa tcaaactact 300
 gccgctgccg ctactgctgc cagtgtgac aacgacgacg acgaggccta ataa 354

<210> 5
 <211> 43
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: ProRIPBF
 primer
 <220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Introduced restriction sites

<400> 5
 actcgagtct agaggatcca tggccgagat aaccctagag ccg 43

<210> 6
 <211> 49
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: ProRIPSR
 primer
 <220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Introduced restriction sites

<400> 6
 gactagtgtc gacgagctct tattaggcct cgtcgtcgtc gttgtcagc 49

<210> 7
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIP1BF primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 7
gctcgagtct agaggatcca tgaaaagaat agtgccaaag ttcactg

47

<210> 8
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIP2SR primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 8
gactagtgtc gacgagctct tattaggcag cggcagtagt ttgattctta acg

53

<210> 9
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIP1SR primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 9
aactagtgtc gacgagctct tattacttct tcttcttcgc caggtcggtg acg

53

<210> 10
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIP2BF primer

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Introduced restriction sites

 <400> 10
 actcgagtct agaggatcca tggcggctga cccacaggcc gacacgaaga g 51

<210> 11
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: RIPCDF primer

<400> 11
 gacctggcga agaagaagaa ggcggctgac ccacaggccg ac 42

<210> 12
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: RIPCDR primer

<400> 12
 gtcggcctgt gggtcagccg ccttcttctt cttcgccagg tc 42

<210> 13
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: RIPSDF primer

<220>
 <221> mutation
 <222> (22)..(27)
 <223> Nucleotides modified to remove SacI site

<400> 13
 ccggagctat ggttctacac agaactgaaa actaggacca gctcc 45

<210> 14
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIPSDR primer

<220>
<221> mutation
<222> (19)..(24)
<223> Nucleotides modified to remove SacI site

<400> 14
ggagctgggc ctagttttca gttctgtgta gaaccatagc tccgg

45

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SUB21 primer

<400> 15
ctcttgcttg aattcggact a

21

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SUB25 primer

<400> 16
tagtccgaat tcaagcaaga gcaca

25

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: LDT15 primer

<400> 17
gacagaagcg gatccttttt tttttttttt

30

<210> 18
<211> 381
<212> DNA
<213> Nicotiana tabacum

<400> 18
 tctagaaagc ttatctaaac aaagtttttaa attcatttct taaacgtcca ttacaatgta 60
 atataactta gtcgtctcaa ttaaaccatt aatgtgaaat ataaatcaaa aaaagccaaa 120
 gggcggtggg acggcgccaa tcatttgtcc tagtccactc aaataaggcc catggtcggc 180
 aaaaccaaac acaaaatgtg ttatttttaa ttttttcctc ttttattgtt aaagttgcaa 240
 aatgtgttat ttttggttaag accctatgga tatataaaga caggttatgt gaaacttgga 300
 aaaccatcaa gttttaagca aaaccctctt aagaacttaa attgagcttc ttttggggca 360
 tttttctagt gagaaggatc c 381

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